

SEQUENCE LISTING

<110> Rosanne M. Crooke
Mark J. Graham

<120> ANTISENSE MODULATION OF MICROSOMAL TRIGLYCERIDE TRANSFER PROTEIN
EXPRESSION

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<211> 20

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<223> Antisense Oligonucleotide

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<212> DNA

<213> Homo sapiens

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Met Ile Leu Leu Ala Val Leu Phe Leu
1 5

tgc ttc att tcc tca tat tca gct tct gtt aaa ggt cac aca act ggt 161
Cys Phe Ile Ser Ser Tyr Ser Ala Ser Val Lys Gly His Thr Thr Gly
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ctc tca tta aat aat gac cgg ctg tac aag ctc acg tac tcc act gaa 209
Leu Ser Leu Asn Asn Asp Arg Leu Tyr Lys Leu Thr Tyr Ser Thr Glu
30 35 40

gtt ctt ctt gat cgg ggc aaa gga aaa ctg caa gac agc gtg ggc tac 257
Val Leu Leu Asp Arg Gly Lys Gly Lys Leu Gln Asp Ser Val Gly Tyr
45 50 55

cgc att tcc tcc aac gtg gat gtg gcc tta cta tgg agg aat cct gat 305
Arg Ile Ser Ser Asn Val Asp Val Ala Leu Leu Trp Arg Asn Pro Asp
60 65 70

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Gly Asp Asp Asp Gln Leu Ile Gln Ile Thr Met Lys Asp Val Asn Val
75 80 85 90 95

75				80				85								
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agc Ser	cca Pro	tct Ser	aaa Lys	ata Ile 110	atg Met	gga Gly	aag Lys	gaa Glu	aac Asn 115	ttg Leu	gaa Glu	gct Ala	ctg Leu	caa Gln 120	aga Arg	449
cct Pro	acg Thr	ctc Leu	ctt Leu 125	cat His	cta Leu	atc Ile	cat His	gga Gly 130	aag Lys	gtc Val	aaa Lys	gag Glu	ttc Phe 135	tac Tyr	tca Ser	497
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agc Ser 155	cta Leu	ttt Phe	cag Gln	aca Thr	cag Gln	tta Leu 160	agc Ser	tct Ser	gga Gly	acc Thr	acc Thr 165	aat Asn	gag Glu	gta Val	gat Asp	593
atc Ile 170	tct Ser	gga Gly	aat Asn	tgt Cys	aaa Lys 175	gtg Val	acc Thr	tac Tyr	cag Gln	gct Ala 180	cat His	caa Gln	gac Asp	aaa Lys	gtg Val 185	641
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acc Thr	acc Thr	tat Tyr 220	aag Lys	ata Ile	gaa Glu	gac Asp	agc Ser 225	ttt Phe	ggt Val	ata Ile	gct Ala	gtg Val 230	ctt Leu	gct Ala	gaa Glu	785
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gcc Ala 410	ctc Leu	att Ile	agt Ser	aag Lys	ttc Phe 415	aaa Lys	ggt Gly	tct Ser	att Ile	ggt Gly 420	agc Ser	agt Ser	gac Asp	atc Ile	aga Arg 425	1361
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Cys Phe Phe Ser Ser Tyr Ser Ala Ser Val Lys Gly His Thr Thr Gly
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Leu Ser Leu Asn Asn Glu Arg Leu Tyr Lys Leu Thr Tyr Ser Thr Glu
30 35 40

gtg ttt ctt gat ggg ggc aaa gga aaa ccg caa gac agc gtg ggc tac 195
Val Phe Leu Asp Gly Gly Lys Gly Lys Pro Gln Asp Ser Val Gly Tyr
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Lys Ile Ser Ser Asp Val Asp Val Val Leu Leu Trp Arg Asn Pro Asp
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Gly Asp Asp Asp Gln Val Ile Gln Val Thr Ile Thr Ala Val Asn Val
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Glu Asn Ala Gly Gln Gln Arg Gly Glu Lys Ser Ile Phe Gln Gly Lys
90 95 100 105

agt aca cct aag atc ata ggg aag gac aac ctg gag gct ctg cag aga 387
Ser Thr Pro Lys Ile Ile Gly Lys Asp Asn Leu Glu Ala Leu Gln Arg
110 115 120

ccc atg ctt ctt cat ctg gtc cgg ggg aag gtc aag gag ttc tac tcc 435
Pro Met Leu Leu His Leu Val Arg Gly Lys Val Lys Glu Phe Tyr Ser
125 130 135

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Tyr Glu Asn Glu Pro Val Gly Ile Glu Asn Leu Lys Arg Gly Leu Ala
140 145 150

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Ser Leu Phe Gln Met Gln Leu Ser Ser Gly Thr Thr Asn Glu Val Asp
155 160 165

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Ile Ser Gly Asp Cys Lys Val Thr Tyr Gln Ala Gln Gln Asp Lys Val
170 175 180 185

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Val Lys Ile Lys Ala Leu Asp Thr Cys Lys Ile Glu Arg Ser Gly Phe
190 195 200

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Ile	Leu	Tyr	Ser	Gly	Ser	Gly	Ile	Leu	Arg	Arg	Ser	Asn	Leu	Asn	Ile	
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ttc	cag	tac	atc	aaa	gga	aca	gag	ctt	cat	ggt	agt	cag	gtg	gtg	att	2019
Phe	Gln	Tyr	Ile	Lys	Gly	Thr	Glu	Leu	His	Gly	Ser	Gln	Val	Val	Ile	
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gag	gag	aac	ctt	gac	tct	tat	gct	ggc	atg	tca	gcc	atc	ctg	ttt	gat	2115
Glu	Glu	Asn	Leu	Asp	Ser	Tyr	Ala	Gly	Met	Ser	Ala	Ile	Leu	Phe	Asp	
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Val	Gln	Leu	Arg	Pro	Val	Thr	Phe	Phe	Asn	Gly	Tyr	Ser	Asp	Leu	Met	
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Ser	Lys	Met	Leu	Ser	Ala	Ser	Gly	Asp	Pro	Val	Ser	Val	Val	Lys	Gly	
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Cys	Met	Gln	Met	Asp	Lys	Ala	Glu	Ala	Pro	Leu	Arg	Gln	Phe	Glu	Thr	
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